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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 18, 2003, 03:18:06 ; Search time 9.6 Seconds
(without alignments)
1581.285 Million cell updates/sec

Title: US-09-807-933B-3

Sequence: 1 MKRTITSSALLALALGTEM.....TYKEVCPKRTAKTGCSRK.366

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues
Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	683.5	33.8	376	1 GUNK_FUSOX	P45699 fusarium ox
2	674	33.4	213	1 GUN5_HUMIN	P43316 humicola in
3	552	27.3	511	1 GUNB_PSEPL	P18126 pseudomonas
4	511.5	25.3	393	1 GUN1_USDMA	P54424 useliago ma
5	238.5	11.8	210	1 PSBP_PORPU	P50272 porphyra pu
6	227.5	11.3	471	1 GUX2_TRIKE	P07982 trichoderma
7	177.5	8.8	438	1 GUX3_AGABI	P49075 agaricus bi
8	167.5	8.3	418	1 GUN2_TRIKE	P07982 trichoderma
9	158.5	7.8	540	1 GUX1_ASAPC	O59843 aspergillus
10	154	7.6	242	1 GUN5_TRIKE	P43317 trichoderma
11	152	7.5	462	1 GUNB_FUSOX	P46236 fusarium ox
12	147.5	7.3	1218	1 JAG1_HUMAN	P78504 homo sapien
13	147.5	7.3	1218	1 JAG1_MOUSE	O98X00 mus musculu
14	145	7.2	485	1 Y136_TREPA	O83172 trepomena p
15	145	7.2	1242	1 JAG3_BRAAE	O90Y54 brachydanio
16	144.5	7.2	1213	1 JAG3_BRAAE	O90Y54 brachydanio
17	144	7.1	442	1 CYS4_DICDI	P54639 dictyosteli
18	143	7.1	385	1 GUNF_FUSOX	P46239 fusarium ox
19	141.5	7.0	1219	1 JAG1_RAT	O63722 rattus norv
20	140.5	7.0	506	1 GUX2_AGABI	O92400 agaricus bi
21	140.5	7.0	713	1 TSA4_GIALA	P12849 giardia lam
22	139.5	6.9	5376	1 ZAN_MOUSE	O88799 mus musculu
23	139	6.9	2704	1 G16B_PARRR	P17053 paramecium
24	135.5	6.7	388	1 GUN3_HUMIN	Q12624 humicola in
25	135	6.7	513	1 GUX1_TRIKE	P19355 trichoderma
26	134	6.6	513	1 GUX1_TRIKE	P00725 trichoderma
27	134	6.6	1202	1 JAG2_RAT	P97607 rattus norv
28	134	6.6	2471	1 NTC2_RAT	O98W30 rattus norv
29	134	6.6	2703	1 NOTC_DROME	P07207 drosophila
30	133.5	6.6	1700	1 BAR3_CHITE	Q03376 chironomus
31	133	6.6	2715	1 G156_PARRR	P13837 paramecium
32	132	6.5	2471	1 NTC2_HUMAN	Q04721 homo sapien
33	129.5	6.4	355	1 YW79_YEAST	Q04018 saccharomyc

34	129.5	6.4	687	1 VS41_GIALA	P92127 giardia lam
35	129	6.4	344	1 GUN4_TRIKE	O14405 trichoderma
36	129	6.4	1246	1 YMW2_CABEL	P34504 caenorhabdl
37	129	6.4	1408	1 SER1_DROME	P18168 drosophila
38	129	6.4	2531	1 NTC1_MOUSE	O01705 mus musculu
39	128.5	6.4	537	1 SP70_DICDI	P15269 dictyosteli
40	128	6.3	667	1 TS11_GIALA	O03185 giardia lam
41	128	6.3	833	1 DL_DROME	P10041 drosophila
42	128	6.3	3712	1 LMA_DROME	O00174 drosophila
43	127.5	6.3	227	1 AGI_ORYSA	P11219 oryza sativ
44	127.5	6.3	316	1 LORI_HUMAN	P23450 homo sapien
45	127.5	6.3	1238	1 JAG2_HUMAN	O9Y219 homo sapien

ALIGNMENTS

RESULT 1
GUNK_FUSOX
ID GUNK_FUSOX STANDARD; PRT; 376 AA.
AC P45699;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Putative endoglucanase type K precursor (EC 3.2.1.4) (Endo-1,4-beta-glucanase) (Cellulase).
OS Fusarium oxysporum.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreales; Mitosporic Hypocreales; Fusarium.
OX NCBI_TaxID=5507;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95047531; PubMed=7959045;
RA Sheppard P.O., Grant F.J., Oort P.J., Sprecher C.A., Foster D.C.,
Hagen F.S., Upshall A., McKnight G.V., O'Hara P.J.;
RT "The use of conserved cellulase family-specific sequences to clone
RT cellulase homologue cDNAs from Fusarium oxysporum.";
RL Gene 150:163-167(1994).
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-glucosidic
CC linkages in cellulose.
CC -1- SIMILARITY: CONTAINS 1 FUNGAL-TYPE CELLULOSE-BINDING DOMAIN (CBD).
CC -1- SIMILARITY: BELONGS TO CELLULASE FAMILY K (FAMILY 45 OF GLYCOSYL
CC HYDROLASES).
CC
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CC
CC -----
CC EMBL: L29381; AAA65589.1; -.
CC HSSP: P43316; ZENG.
CC InterPro: IPR000254; CBD fungal.
CC InterPro: IPR000334; GH_45.
CC Pfam: PF00734; CBM_1; 1_1_45.
CC Pfam: PF02015; Glyco_hydro_45; 1.
CC SMART: SM00236; ECBD; 1.
CC PROSITE: PS00562; CBD_FUNGAL; 1.
CC PROSITE: PS01140; GLYCOSYL_HYDROL_F45; 1.
CC KEGG: Cellulose degradation; Hydrolyase; Glycosidase; Signal.
CC SIGNAL 1 18
CC CHAIN 19 376
CC DOMAIN 19 308
CC DOMAIN 309 338
CC DOMAIN 339 376
CC ACT_SITE 29 29
CC ACT_SITE 140 140
CC SEQUENCE 376 AA; 39235 MW; B430A5F962B9F882 CRC64;
Query Match 33.8%; Score 683.5; DB 1; Length 376;
Best Local Similarity 57.1%; Pred. No. 1.2e-38;

Matches 120; Conservative 34; Mismatches 49; Indels 7; Gaps 4;

QY 157 ASGNVTTRVMDCCASGSPGKANVSPVSKCNKDVLTALSDSNVSGCNGNS-YWGN 215
 DB 18 ASGSHSTRVMDCCASGSPGKANVSPVSKCNKDVLTALSDSNVSGCNGNS-YWGN 76
 QY 216 DNQPAVNDNLAYGAAALISGGESRWCCSCFELTFTSTSVAGKKNVIQVNTGDLGS 275
 DB 77 NYSFPAVNDNLAYGAAALISGGESRWCCSCFELTFTSTSVAGKKNVIQVNTGDLGS 136
 QY 276 SGAHFDLQMPGGGAGIFNGSKWGA-PNDGMSRRYGGISSASDSSLPSALQAGCKMRF 335
 DB 137 N---HFDLMPGGGAGIFNGSKWGA-PNDGMSRRYGGISSASDSSLPSALQAGCKMRF 191
 QY 336 NMFKNADNPMTYKEVTCPEKRTAKTGCSR 365
 DB 192 DMFENADNPMTYKEVTCPEKRTAKTGCSR 221

RESULT 2

GUNS_HUMIN STANDARD; PRT; 213 AA.

AC P43316;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Endoglucanase V (EC 3.2.1.4) (Endo-1,4-beta-glucanase V)
 DB (Cellulase V) (EG V).
 OS Humicola insolens.
 OC Eukaryota; Fungi; Ascomycota; mitosporic Ascomycota; Humicola.
 NX NCBI_TaxID=34413;
 RN (1)
 RP SEQUENCE FROM N.A.
 RA Rasmussen G., Mikkelsen J.-M., Schuelein M., Packar S.A., Hagen F.,
 RA Hjort C.M., Hestrup S.;
 RT "A cellulase preparation comprising an endoglucanase enzyme.";
 RL Patent number WO9117243, 14-NOV-1991.
 RN (2)
 RP X-RAY CRYSTALLOGRAPHY (1.6 ANGSTROMS).
 RX MEDLINE=93390621; PubMed=8377830;
 RA Davies G.J., Dodson G.G., Hubbard R.E., Tolley S.P., Dauter Z.,
 RA Wilson K.S., Hjort C., Mikkelsen J.M., Rasmussen G., Schuelein M.;
 RT "Structure and function of endoglucanase V.";
 RL Nature 363:362-364 (1993).
 RN (3)
 RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
 RX MEDLINE=96101453; PubMed=8519779;
 RA Davies G.J., Tolley S.P., Hentissat B., Hjort C., Schuelein M.;
 RT "Structures of oligosaccharide-bound forms of the endoglucanase V
 from Humicola insolens at 1.9-A resolution.";
 RL Biochemistry 34:16210-16220 (1995).
 RN (4)
 RP X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS).
 RA Davies G.J., Dodson G.G., Moore M.H., Tolley S.P., Dauter Z.,
 RA Wilson K.S., Rasmussen G., Schuelein M.;
 RT "Structure determination and refinement of the Humicola insolens
 endoglucanase V at 1.5-A resolution.";
 RL Acta Crystallogr. D 52:7-17 (1996).
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-glucosidic
 linkages in cellulose.
 CC -1- SIMILARITY: BELONGS TO CELLULOSE FAMILY K (FAMILY 45 OF GLYCOSYL
 HYDROLASES).
 CC PDB; 2ENG; 08-DEC-96.
 DR PDB; 3ENG; 16-JUN-97.
 DR PDB; 4ENG; 16-JUN-97.
 DR InterPro; IPR000334; GH_45.
 DR Pfam; PF02015; Glyco_hydro_45; 1.
 DR PROSITE; PS01140; GLYCOSYL_HYDROL_45; 1.
 DR Cellulose degradation; Hydrolyase; Glycosidase; 3D-structure.
 FT ACT SITE 10 10 NUCLEOPHILE.
 FT ACT SITE 121 121 PROTON DONOR.
 SQ SEQUENCE 213 AA; 22864 MW; 24334301BA3BC804 CRC64;

Query Match 33.4%; Score 674; DB 1; Length 213;
 Best Local Similarity 58.2%; Pred. No. 3e-38;
 Matches 121; Conservative 32; Mismatches 45; Indels 10; Gaps 5;

QY 160 NGVTRVMDCCASGSPGKANVSPVSKCNKDVLTALSDSNVSGCNGN-IGNSYMCNDQ 218
 DB 2 DGRSTRVMDCCASGSPGKANVSPVSKCNKDVLTALSDSNVSGCNGN-IGNSYMCNDQ 60
 QY 219 FPAVNDNLAYGAAALISGGESRWCCSCFELTFTSTSVAGKKNVIQVNTGDLGSSTG 278
 DB 61 FPAVNDNLAYGAAALISGGESRWCCSCFELTFTSTSVAGKKNVIQVNTGDLGSSTG 118
 QY 279 AHFDLQMPGGGAGIFNGSKWGA-PNDGMSRRYGGISSASDSSLPSALQAGCKMRF 337
 DB 119 -HFDLMPGGGAGIFNGSKWGA-PNDGMSRRYGGISSASDSSLPSALQAGCKMRF 173
 QY 338 NMFKNADNPMTYKEVTCPEKRTAKTGCSR 365
 DB 174 FMKNADNPMTYKEVTCPEKRTAKTGCSR 201

RESULT 3

GUNB_PSEFL STANDARD; PRT; 511 AA.

AC P18126;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Endoglucanase B precursor (EC 3.2.1.4) (Endo-1,4-beta-glucanase)
 DB (Cellulase) (EGB).
 OS CELB.
 OS Pseudomonas fluorescens.
 OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
 OC Pseudomonas.
 NX NCBI_TaxID=294;
 RN (1)
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 30-48.
 RC STRAIN=Sp. Cellulosa;
 RX MEDLINE=90355836; PubMed=2117693;
 RA Gilbert H.J., Hall J., Hazlewood G.P., Ferreira L.M.A.;
 RT "The N-terminal region of an endoglucanase from Pseudomonas
 fluorescens subspecies cellulosa constitutes a cellulose-binding
 domain that is distinct from the catalytic centre.";
 RL Mol. Microbiol. 4:759-767 (1990).
 CC -1- FUNCTION: THIS ENZYME CATALYZES THE ENDOHYDROLYSIS OF 1,4-BETA-
 GLUCOSIDIC LINKAGES IN CELLULOSE, LICHENIN AND CEREAL BETA-D-
 GLUCANS. EGB IS MOST ACTIVE AGAINST BARLEY BETA-GLUCAN, BUT SHOWED
 SIGNIFICANT ACTIVITY AGAINST AMORPHOUS AND CRYSTALLINE CELLULOSE.
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-glucosidic
 linkages in cellulose.
 CC -1- SUBCELLULAR LOCATION: Periplasmic.
 CC -1- SIMILARITY: CONTAINS 1 BACTERIAL-TYPE CELLULOSE-BINDING DOMAIN
 (CBD).
 CC -1- SIMILARITY: BELONGS TO CELLULOSE FAMILY K (FAMILY 45 OF GLYCOSYL
 HYDROLASES).
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 or send an email to license@isb.ch).
 CC EMBL; X52615; CAA36844.1; -.
 DR PIR; S10527; S10527.
 DR HSP; P43316; 2ENG.
 DR InterPro; IPR001919; Bac celose-bind.
 DR InterPro; IPR002883; CBD_5.
 DR InterPro; IPR000334; GH_45.
 DR Pfam; PF00553; CBM_2; 1.
 DR Pfam; PF02013; CBM_10; 1.
 DR Pfam; PF02015; Glyco_hydro_45; 1.

DR PROSITE: PS00561; CBD BACTERIAL; 1.
 DR PROSITE: PS01140; GLYCOSYL HYDROL_P45; 1.
 KW Cellulose degradation; Hydrolase; Glycosidase; Signal; Periplasmic.
 FT SIGNAL 1 29
 FT CHAIN 30 511
 FT DOMAIN 30 131
 FT DOMAIN 132 173
 FT DOMAIN 223 259
 FT DISULFID 32 127
 FT ACT_SITE 276 276
 FT ACT_SITE 393 393
 SQ SEQUENCE 511 AA; 52078 MM; 3C3119D998291D8E CRC64;
 Query Match 27.3%; Score 552; DB 1; Length 511;
 Best Local Similarity 34.0%; Pred. No. 8.2e-30;
 Matches 139; Conservative 56; Mismatches 136; Indels 78; Gaps 16;
 QY 17 GTENASAKSKLYGO-CGGKDMNGPT--CCESGSTCKVNDYVSOCLAPESN--GNKKS 71
 DB 110 GNNSSRAQVAVTGAICGGGSSAPSSVSSSSSVSTPRSSSSSVSVPTSSS 169
 QY 72 ECKLYGCGCGKDMNG--PTC-----CESGSTCKVNDYVSOCLAPESNG 114
 DB 170 SSSSVLTGAQACNMYGTLTPLCNNTSNGWGEDGRSCVARTTCSAOPAPYIVSTSSSTP 229
 QY 115 NKTESAHKTTTTPAKKEITTTAKASNSNSGKYSIVSGASGNGVTTHYMOCKKASC 174
 DB 230 LSSSSSSSVSSVSSSSSSAT--SSSASSSVSPPTDGC--NGATRYMPCCKPHC 282
 QY 175 SWPKANVS---SPVSKCNKDGVTALSDSNVQSGCNGNSYKCNNDQPMVANDILAYGA 231
 DB 283 GW--SAVPSLVSPVSGSANN--TSLSVSVSGSCDGGGGMCKDIPFASPTLAYGA 339
 QY 232 AAISGGESRWCCSCFELTIT--STSVAGKKMVTQVNTGSDLSSTGAH 280
 DB 340 ATS--SGD---VCRCYLOLFTGSSYNAPDPSALALAKTMIYQATNIGYDV--SGGQ 391
 QY 281 FDLMPGGGVIPIFGCSKQMGAPNDGSRGGYSSA-----SDCS 321
 DB 392 FDLVPGGGAFAFNACSNQMGVSNALQAYGGFLAAKQQLCVNASLSQYKCVLNRCD 451
 QY 322 SL-----PSALQAGCKMRFNFKNADNPMYKEVTCPEKITPAKTCGR 365
 DB 452 SVFSGRLTQLOGGCTWFAWFEADNPLSKYKEVPCALITTSQNR 500
 RESULT 4
 GUNI_USTMA STANDARD; PRT; 393 AA.
 ID GUNI_USTMA
 AC P54424;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE Endoglucanase 1 precursor (EC 3.2.1.4) (Endo-1,4-Beta-glucanase 1)
 DE (Cellulase 1) (EG 1).
 GN EGL1
 OS Ustilago maydis (Smut fungus).
 OC Eukaryota; Fungi; Basidiomycota; Ustilaginomycetes;
 OC Ustilaginomycetidae; Ustilaginales; Ustilaginaceae; Ustilago.
 OX NCBI_TaxID=5270;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FBD11;
 RX MEDLINE=96145728; PubMed=8590631;
 RA Schaevecker F., Wanner G., Kahmann R.;
 RT "Filament-specific expression of a cellulase gene in the dimorphic
 RT fungus Ustilago maydis";
 RT Biol. Chem. Hoppe-Seyler 376:617-625(1995).
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-glucosidic
 CC linkages in cellulose.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: HYPHAL TIP.
 CC -1- DEVELOPMENTAL STAGE: EXPRESSED IN FILAMENTOUS DIKARYON.

CC -1- PTM: MAY ALSO BE O-GLYCOSYLATED.
 CC -1- SIMILARITY: BELONGS TO CELLULASE FAMILY K (FAMILY 45 OF GLYCOSYL
 CC HYDROLASES).
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 CC
 CC EMBL; S81598; AAB36147.1; -
 DR HSPB_P43316; ZENG.
 DR InterPro: IPR000334; GH_45.
 DR Pfam: PF02015; Glyco_hydro_45; 1.
 DR PROSITE: PS01140; GLYCOSYL HYDROL_P45; 1.
 KW Cellulose degradation; Hydrolase; Glycosidase; Signal; Glycoprotein.
 FT SIGNAL 1 26
 FT CHAIN 27 393
 FT ACT_SITE 34 34
 FT ACT_SITE 152 152
 FT DOMAIN 270 385
 FT CARBOHYD 343 343
 SQ SEQUENCE 393 AA; 39594 MM; 65C753C610CD6AD3 CRC64;
 Query Match 25.3%; Score 511.5; DB 1; Length 393;
 Best Local Similarity 47.0%; Pred. No. 3.1e-27;
 Matches 103; Conservative 30; Mismatches 65; Indels 21; Gaps 9;
 QY 161 GVTTRYNDCCASGWPCKANVSSPVKCNKDGVTAL--SDSNVQSGCNGNSYKCNNDN 217
 DB 27 GMATRYNDCCIASGWPCKAPVAPVADCKADGVTLLDSKDPGSGGSCNGNFMKSCM 86
 QY 218 QPW--AVNDILAYGAFAAASGGESRWCCSCFELTIT--STSVAGKKMVTQVNTG 271
 DB 87 QPFDFTDPTLAFGF--GAFTTQGESDTCACFYAEFEHDAQKAMRNKTLIPVTTWVG 144
 QY 272 DLGSGTAHPLQMPGGGVIPIFGCSKQMGAPNDGSRGGYSSA-----SDCS 321
 DB 145 DVQSQ--NFDFOIPGGGLAFPRGCPAQMGVSNALQAYGGFLAAKQQLCVNASLSQYKCVLNRCD 451
 QY 331 CKMRFN--WPKNADNPM--TYKEVTCPEKITPAKTCGR 366
 DB 202 CKMRFSEW--GDNPVLKGSFPRKVCRLIDRSGCGRK 237
 RESULT 5
 PSBP_PORPU STANDARD; PRT; 210 AA.
 ID PSBP_PORPU
 AC P50272;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Putative polysaccharide binding protein precursor.
 DE Porphyra purpurea.
 OC Eukaryota; Rhodophyta; Bangiophyceae; Bangiales; Bangiaceae; Porphyra.
 OX NCBI_TaxID=2787;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Avonport;
 RA Liu Q., der Meer J.P., Reith M.E.;
 RL Submitted (MAR-1994) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: CONTAINS 4 FUNGAL-TYPE CELLULOSE-BINDING DOMAINS
 CC (CBD).
 CC
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CC EMBL; U08843; AAA61792.1; -
DR HSSP; P00725; 2CBH.
DR InterPro; IPR000254; CBD_fungal.
DR Pfam; PF00734; CBM_1; 4.
DR SMART; SM00236; fCBM; 4.
DR PROSITE; PS00562; CBD_FUNGAL; 4.
KM Repeat; signal.
FT SIGNAL 1 22
FT CHAIN 23 210 PUTATIVE POLYSACCHARIDE BINDING PROTEIN.
FT DOMAIN 23 105 POLYSACCHARIDE BINDING DOMAIN I.
FT DOMAIN 63 105 POLYSACCHARIDE BINDING DOMAIN II.
FT DOMAIN 125 165 POLYSACCHARIDE BINDING DOMAIN III.
FT DOMAIN 166 210 POLYSACCHARIDE BINDING DOMAIN IV.
SQ SEQUENCE 210 AA; 21967 MW; 837822D98B6863C8 CRC64;

Query Match 11.8%; Score 238.5; DB 1; Length 210;
Best Local Similarity 28.5%; Pred. No. 2e-09;
Matches 73; Conservative 25; Mismatches 95; Indels 63; Gaps 11;

QY 1 MKFTITSSALALALGTEMASAAKSKLYGCGGKDMNPGTCESGSGTCVSNQYSGC 60
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 1 MGLKGTAAALTLISA--AAASAGCVLEQGGIGFDGTCSEGLMCMKMGPIYSQC 57
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 61 LA-PESNGKSSSECSKLYGCGGKDMNPGTCESGSGTCVSNQYSGCLAPESNGKTS 119
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 58 RAMPGMGQ---VAPYCGCGGMNYSKTMCSPGFKCVLELNFESQC---DLANKSPV 108
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 120 SAHKTITTTAPAKETTTAKASNSNSGKTSVSGGAGANGVTIRYMCKC-----A 172
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 109 APTKVAPTSP-----GPAQVCGEYVAACGEMFWGA---KCCFGLVCYET 152
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 173 SCSPGKAVNSPVKSCNKGVTALSDSNVSGCNGANSY---MCNDQPAVNDNLAY 228
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 153 SGWQSGCCRAPPP-----KMEVGRYAC-GGMKMGSTMC-----VG 189
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
QY 229 GFAAAIISGGESRMC 244
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 190 GYKMAISGSMYKQC 205
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

RESULT 6
ID GUX2 TRIRE STANDARD; PRT; 471 AA.
AC P07987;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Exoglucanase II precursor (EC 3.2.1.91) (Exocellulohydrolase II)
DE (CBHI) (1,4-beta-cellobiohydrolase).
GN CBH2.
OS Trichoderma reesei (Hypocrea jecorina).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreales; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC NCBI_TaxID=51453;
OX NCBI_TaxID=51453;
RN 1
RP SEQUENCE FROM N.A.
RC STRAIN=VTT-D-80133;
RX MEDLINE=87248061; PubMed=3596237;
RA Teeri T.T., Lehtovaara P., Kauppinen S., Salovuori I., Knowles J.;
RT "Homologous domains in Trichoderma reesei cellulolytic enzymes: gene
   sequence and expression of cellobiohydrolase II.",
   Gene 51:43-52 (1987).
RL 12
RN 12
RP SEQUENCE FROM N.A.
RC STRAIN=QM9414 / Rut C-30;
RA Chen C.W., Gritzali M., Staflford D.W.;
RT "Nucleotide sequence and deduced primary structure of
   cellobiohydrolase II from Trichoderma reesei.",
   Biotechnology 5:274-278 (1987).
RL 13
RN 13
RP SEQUENCE OF 25-44.
RA Paegerstam L.G., Petersson L.G.;

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RT "The 1,4-beta-glucan cellobiohydrolases of Trichoderma reesei QM
   9414.",
   FEBS Lett. 119:97-100(1980).
RL 14
RN 14
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RX MEDLINE=90333255; PubMed=2377899;
RA Rouvinen J., Bergfors T., Teeri T.T., Knowles J.K.C., Jones T.A.;
RT "Three-dimensional structure of cellobiohydrolase II from Trichoderma
   reesei.",
   Science 249:380-386 (1990).
RN 15
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RX MEDLINE=97029636; PubMed=8875646;
RA Koivula A., Reinikainen T., Ruohonen L., Valkeajarvi A., Rouvinen J.,
   Claessens M., Teeman O., Kleywegt G.J., Szardenings M., Rouvinen J.,
   Jones T.A., Teeri T.T.;
RA "The active site of Trichoderma reesei cellobiohydrolase II: the role
   of tyrosine 169.",
   Protein Eng. 9:691-699(1996).
RL 16
RN 16
RP FUNCTION: THE BIOLOGICAL CONVERSION OF CELLULOSE TO GLUCOSE
CC -1- GENERALLY REQUIRES THREE TYPES OF HYDROLYTIC ENZYMES:
CC (1) ENDOGLUCANASES WHICH CUT INTERNAL BETA-1,4-GLUCOSIDIC BONDS;
CC (2) EXOCELLULOBIOSYLASES THAT CUT THE DISSACCHARIDE CELLOBIOSE
CC FROM THE NONREDUCING END OF THE CELLULOSE POLYMER CHAIN;
CC (3) BETA-1,4-GLUCOSIDASES WHICH HYDROLYZE THE CELLOBIOSE AND OTHER
CC SHORT CELLO-OLIGOSACCHARIDES TO GLUCOSE.
CC -1- CATALYTIC ACTIVITY: Hydrolyzes of 1,4-beta-D-glucosidic linkages
CC in cellulose and cellotetraose, releasing cellobiose from the non-
CC reducing ends of the chains.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- MISCELLANEOUS: T. RESEI PRODUCES TWO DIFFERENT
CC EXOCELLULOBIOSYLASES. THEY ARE UNIQUE IN THAT THEY CAN HYDROLYSE
CC CRYSTALLINE CELLULOSE IN THE ABSENCE OF ENDOGLUCANASES
CC -1- SIMILARITY: BELONGS TO CELLULASE FAMILY B (FAMILY 6 OF GLYCOSYL
CC HYDROLASES).
CC -1- SIMILARITY: CONTAINS 1 FUNGAL-TYPE CELLULOSE-BINDING DOMAIN (CBD).
CC -----
CC DR EMBL; M16190; AAA4210.1; -
CC DR EMBL; M55080; AAA72922.1; -
CC DR PIR; A26472; A26472.
CC DR PIR; A26160; A26160.
CC DR PDB; 3CBH; 15-JAN-91.
CC DR PDB; 1CB2; 19-MAR-93.
CC DR InterPro; IPR000254; CBD_fungal.
CC DR InterPro; IPR001524; GH_6.
CC DR Pfam; PF00734; CBM_1; 1.
CC DR Pfam; PF01341; GHYDRO_6; 1.
CC DR PRINTS; PR00733; GHYDRLASE6.
CC DR PRODOM; PD001821; CBD_fungal; 1.
CC DR PRODOM; PD003733; GH_6; 1.
CC DR SMART; SM00236; fCBM; 1.
CC DR PROSITE; PS00562; CBD_FUNGAL; 1.
CC DR PROSITE; PS00655; GLYCOSYL_HYDROL_F6_1; 1.
CC DR PROSITE; PS00656; GLYCOSYL_HYDROL_F6_2; 1.
CC DR "Cellulose degradation; Hydrolase; Glycosidase; Glycoprotein; Signal;
   3D-structure.
KM 3D-structure. 1 24
FT SIGNAL 25 471 EXOGLUCANASE II.
FT CHAIN 25 471 CELLULOSE-BINDING (BY SIMILARITY).
FT DOMAIN 25 65 LINKER.
FT DOMAIN 66 106 CATALYTIC.
FT DOMAIN 107 471 CATALYTIC.
FT ACT_SITE 199 199 PROTON DONOR.
FT ACT_SITE 245 245 NUCLEOPHILE.
FT ACT_SITE 425 425 BY SIMILARITY.
FT DISULFID 34 51

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FT DISULFID 45 61 BY SIMILARITY.
FT DISULFID 200 259
FT DISULFID 392 439
FT CARBOHYD 38 38 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 111 111 O-LINKED (MAN. . .)
FT CARBOHYD 121 121 O-LINKED (MAN. . .)
FT CARBOHYD 130 130 O-LINKED (MAN. . .)
FT CARBOHYD 133 133 O-LINKED (MAN. . .)
FT CARBOHYD 134 134 O-LINKED (MAN. . .)
FT CARBOHYD 139 139 O-LINKED (MAN. . .)
FT CARBOHYD 313 313 N-LINKED (GLCNAC. . .)
FT CARBOHYD 334 334 N-LINKED (GLCNAC. . .)
FT MUTAGEN 199 199 D->A: 20% OF WILD-TYPE ACTIVITY.
FT MUTAGEN 245 245 P->A: NO MEASURABLE ACTIVITY.
FT CONFLICT 359 359 P->A: R (IN REF. 2).
FT CONFLICT 449 449 P->A: A (IN REF. 2).
SQ SEQUENCE 471 AA; 49653 MW; C471B035B1BD8 CRC64;

Query Match 11.3%; Score 227.5; DB 1; Length 471;
Best Local Similarity 22.7%; Pred. No. 2.3e-08;
Matches 113; Conservative 38; Mismatches 159; Indels 187; Gaps 22;

QY 4 ITTSSALLALALCTEMASAKSKLYGCGCGKDMNGPTCCSGSTCKVSNDRYSQCLAP 63
DB 5 ILTLATLATLATAVPLEERQACSSVMGCGCGKDMNGPTCCSGSTCKVSNDRYSQCLAP 64
QY 64 ESNKNSKSECKLYGCGCGKDMNGPTCCSGS-----TCRY----- 99
DB 65 AASSSSSTRASTSTRV-----SPTTSRSSATPPPGSTTTPVPGSGTATYSQNPV 118
QY 100 -----SNDY-----SCLAPESNGNKTSESA-----HKTITTAPEKIT 136
DB 119 GVTPMANAYVASEVSLAPSLTGAMATAAAVAKVPSFMWLTPLDRTPLMEQTLADIRT 178
QY 137 TAKASNSN-----SGKTSIVSGGASG-----NGVTRTWDC 169
DB 179 ANK--NGGNVAGQFVVYDLPDRDCAALASNEYSIADGKVAKYNYIDTIRQIVVEYSDI 236
QY 170 -----CKASGWPGRKANVSFVASCNKDGTALSDSNVSGCGNGSYMND 216
DB 237 RTLLVIEPDSLANTVTNIGTKCANAGSAYIECTINVAITOLNLPVAMVYLDAGHAGWLG- 295
QY 217 NQPMVNDNLAYGFPAALISGGGSESR-----WCCSCFELTFTSTVAGKRM 262
DB 296 ---WPAQDPAAQLEFANYKYKASSPRALGLATVNAVANGNITSPSPYTGNAVYMEKL 352
QY 263 VIO-----VTNTG-----GDLSSSTGAHFDLQPGGSGVIFNGCSKRWG- 301
DB 353 YIHAIGPLLANHGMNSNAFPTDQGRSG-----KQPTG-----QQQWDMCNVIGTG 398
QY 302 ---APRDG-----WGSRYGISASDCS-----SLPSAL-----QAGCKRKN 336
DB 399 FGIRPSANTGSLDPSFVWVRGEGCDGSDSAPRFDSCALPDALQAPADAGA----- 453
QY 337 WFK-----NADNPS 345
DB 454 WFOAYFVQQLTNA-NPS 469

RESULT 7
GUX3_AGABI STANDARD; PRT; 438 AA.
AC PA9075;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-JUN-1999 (Rel. 38, Last annotation update)
DE Exoglucanase 3 precursor (EC 3.2.1.91) (Exocellulohydrolase 3)
DE (1,4-beta-cellulohydrolase 3).
GN CEL3
OS Agaricus bisporus (Common mushroom).
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
OC Agaricales; Agaricaceae; Agaricus.
OC NCBI_TaxID=5341;

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```

RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 255-277 AND 331-351.
RC STRAIN=D649;
RX MEDLINE=94368092; PubMed=8085821;
RA Chow C.-M., Yague E., Raguz S., Wood D.A., Thurston C.F.;
RT "The cell gene of Agaricus bisporus codes for a modular cellulase and
RL is transcriptionally regulated by the carbon source.";
RN Appl. Environ. Microbiol. 60:2779-2785(1994).
[2]
RP SEQUENCE FROM N.A.
RC TISSUE=Mycelium;
RX MEDLINE=96269930; PubMed=8662210;
RA Yague E., Chow C.-M., Challen M.P., Thurston C.F.;
RT "Correlation of exons with functional domains and folding regions in
RL a cellulase from Agaricus bisporus.";
RN Curr. Genet. 30:56-61(1996).
CC -1- FUNCTION: SHOWS ENZYMIC ACTIVITY TOWARDS CRYSTALLINE CELLULOSE.
CC AT LONG REACTION TIMES. IT IS ALSO ABLE TO DEGRADE CARBOXYMETHYL
CC CELLULOSE AND BARLEY B-GLUCAN.
CC -1- CATALYTIC ACTIVITY: Hydrolysis of 1,4-beta-D-glucosidic linkages
CC in cellulose and cellotetraose, releasing cellobiose from the non-
CC reducing ends of the chains.
CC -1- SIMILARITY: BELONGS TO CELLULASE FAMILY B (FAMILY 6 OF GLYCOSYL
CC HYDROLASES).
CC -1- SIMILARITY: CONTAINS 1 FUNGAL-TYPE CELLULOSE-BINDING DOMAIN (CBD).
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; L24519; AAA50607.1; -
DR EMBL; L24520; AAA50608.1; -
DR EMBL; Z34007; CA83971.1; -
DR HSSP; P00725; 1A26.
DR InterPro; IPR000254; CBD_fungal.
DR InterPro; IPR001524; GH_6.
DR Pfam; PF00734; CBM_1; 1.
DR Pfam; PF01341; Glyco_hydro_6; 1.
DR PRINTS; PR00733; GLHYDRLABE6.
DR ProDom; PD001821; CBD_fungal; 1.
DR ProDom; PD003733; GH_6; 1.
DR SMART; SM00236; ECBD; 1.
DR PROSITE; PS00562; CBD_FUNGAL; 1.
DR PROSITE; PS00655; GLYCOSYL_HYDROL_F6_1; 1.
DR PROSITE; PS00656; GLYCOSYL_HYDROL_F6_2; 1.
KW Cellulose degradation; Hydrolase; Glycosidase; Signal.
FT SIGNAL 1 20
FT CHAIN 21 438 EXOGLUCANASE 3.
FT DOMAIN 21 59 CELLULOSE-BINDING (BY SIMILARITY).
FT DOMAIN 60 87 LINKER.
FT DOMAIN 88 438 CATALYTIC.
FT ACT_SITE 215 215 PROTON DONOR (BY SIMILARITY).
FT ACT_SITE 393 393 NUCLEOPHILE (BY SIMILARITY).
FT DISULFID 28 45 BY SIMILARITY.
FT DISULFID 39 55 BY SIMILARITY.
FT DISULFID 170 229 BY SIMILARITY.
FT DISULFID 360 407 BY SIMILARITY.
FT VARIANT 133 133 V->T.
FT VARIANT 152 152 R->Q.
FT VARIANT 244 244 V->I.
FT VARIANT 248 248 N->D.
FT VARIANT 398 398 N->S.
SQ SEQUENCE 438 AA; 46209 MW; 002C973544893794 CRC64;

Query Match 8.8%; Score 177.5; DB 1; Length 438;
Best Local Similarity 24.7%; Pred. No. 4.4e-05;
Matches 107; Conservative 41; Mismatches 151; Indels 135; Gaps 21;

QY 9 SALLALAL---GTEMASAKSKLYGCGCGKDMNGPTCCSGSTCKVSNDRYSQCL----- 61

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CC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 CC Eucotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
 CC NCBI_TaxID=5053;
 CC [1]
 CC SEQUENCE FROM N.A.
 CC STRAIN=F-50;
 CC Takada G., Kawaguchi T., Sumitani J., Arai M.;
 CC "Cloning, nucleotide sequence, and transcriptional analysis of
 CC *Aspergillus aculeatus* No.F-50 cellobiohydrolase I (chil) gene.",
 CC J. Ferment. Bioeng. 85:1-9(1998).
 CC -1- FUNCTION: THE BIOLOGICAL CONVERSION OF CELLULOSE TO GLUCOSE
 CC GENERALLY REQUIRES THREE TYPES OF HYDROLYTIC ENZYMES:
 CC (1) ENDOLUCANASES WHICH CUT INTERNAL BETA-1,4-GLUCOSIDIC BONDS;
 CC (2) EXOCELLULOSEHYDROLASES THAT CUT THE DISACCHARIDE CELLULOSE
 CC FROM THE NONREDUCING END OF THE CELLULOSE POLYMER CHAIN;
 CC (3) BETA-1,4-GLUCOSIDASES WHICH HYDROLYZE THE CELLULOSE AND OTHER
 CC SHORT CELLO-OLIGOSACCHARIDES TO GLUCOSE.
 CC -1- CATALYTIC ACTIVITY: Hydrolysis of 1,4-beta-D-glucosidic linkages
 CC in cellulose and celloetraose, releasing cellobiose from the non-
 CC reducing ends of the chains.
 CC -1- SIMILARITY: BELONGS TO CELLULOSE FAMILY C (FAMILY 7 OF GLYCOSYL
 CC HYDROLASES).
 CC -1- SIMILARITY: CONTAINS 1 FUNGAL-TYPE CELLULOSE-BINDING DOMAIN (CBD).
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; AB002821; BAA25183.1; -
 CC HSSP; P00725; 1A26.
 CC InterPro; IPR000254; CBD_fungal.
 CC InterPro; IPR001722; GH_7.
 CC Pfam; PF00734; CBM_1; 1.
 CC Pfam; PF00840; Glyco_hydro_7; 1.
 CC ProDom; PD001821; CBD_fungal; 1.
 CC ProDom; PD186135; GH_7; 1.
 CC SMART; SM00236; FCB; 1.
 CC PROSITE; PS00562; CBD_FUNGAL; FALSE NEG.
 CC PROSITE; PS01140; GLYCOSYL_HYDROL_F45; 1.
 CC Cellulose degradation; Hydrolase; Glycosidase; Glycoprotein; Signal.
 CC KW SIGNAL 1 22
 CC CHAIN 23 540
 CC DOMAIN 23 459
 CC DOMAIN 460 505
 CC ACT_SITE 234 234
 CC ACT_SITE 239 239
 CC DISULFID 524 539
 CC CARBOHYD 434 434
 CC CARBOHYD 458 458
 CC SEQUENCE 540 AA; 57099 MW; 002D7FD28DF194D0 CRC64;
 CC
 CC Query Match 7.8%; Score 158.5; DB 1; Length 540;
 CC Best Local Similarity 41.3%; Pred. No. 0.00096;
 CC Matches 31; Conservative 9; Mismatches 34; Indels 1; Gaps 1;
 CC
 CC QY 34 GAKDMNGPTCCSGSTCKVSNQCLAPESNGKSECSKLYGCGCGKDMNGPTCCS 93
 CC DB 467 GGGSSSTLTTLTKASTSTSTSTSTSTSTSTSTSTSTSTSTSTSTSTSTST 526
 CC QY 94 GSTCKVSNQCL 108
 CC DB 527 G-TCTKNDYYSQCL 540
 CC
 CC RESULT 10
 CC GUNB_TRIRE STANDARD; PRT; 242 AA.
 CC AC P43317;

DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Endoglucanase V precursor (EC 3.2.1.4) (Endo-1,4-beta-glucanase V)
 DE (Cellulase V) (EG V).
 GN EGL5.
 OS Trichoderma reesei (Hypocrea jecorina).
 CC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 CC Hypocreales; Hypocreaaceae; Hypocrea.
 CC NCBI_TaxID=51453;
 CC [1]
 CC SEQUENCE FROM N.A.
 CC STRAIN=QM9414 / Rut C-30;
 CC MEDLINE=95075308; Pubmed=7984103;
 CC Salohimo A., Henriksas B., Hoffman A.-M., Penttilae M.;
 CC "A novel, small endoglucanase gene, egl5, from Trichoderma reesei
 CC isolated by expression in yeast.",
 CC Mol. Microbiol. 13:219-228(1994).
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-glucosidic
 CC linkages in cellulose.
 CC -1- SIMILARITY: BELONGS TO CELLULOSE FAMILY K (FAMILY 45 OF GLYCOSYL
 CC HYDROLASES).
 CC -1- SIMILARITY: CONTAINS 1 FUNGAL-TYPE CELLULOSE-BINDING DOMAIN (CBD).
 CC -----
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; Z33381; CAA83846.1; -
 CC HSSP; P00725; 2CBH.
 CC InterPro; IPR000254; CBD_fungal.
 CC InterPro; IPR001344; GH_45.
 CC Pfam; PF00734; CBM_1; 1.
 CC Pfam; PF02015; Glyco_hydro_45; 1.
 CC ProDom; PD001821; CBD_fungal; 1.
 CC SMART; SM00236; FCB; 1.
 CC PROSITE; PS00562; CBD_FUNGAL; 1.
 CC PROSITE; PS50842; EXPANSIN_EG45; 1.
 CC PROSITE; PS01140; GLYCOSYL_HYDROL_F45; 1.
 CC Cellulose degradation; Hydrolase; Glycosidase; Signal.
 CC KW SIGNAL 1 17
 CC CHAIN 18 242
 CC DOMAIN 27 27
 CC ACT_SITE 134 134
 CC ACT_SITE 182 182
 CC DOMAIN 183 205
 CC DOMAIN 206 242
 CC CARBOHYD 182 182
 CC DISULFID 213 230
 CC DISULFID 224 240
 CC SEQUENCE 242 AA; 24411 MW; CC033FC51326C7AD CRC64;
 CC
 CC Query Match 7.6%; Score 154; DB 1; Length 242;
 CC Best Local Similarity 40.5%; Pred. No. 0.0009;
 CC Matches 32; Conservative 10; Mismatches 29; Indels 8; Gaps 2;
 CC
 CC QY 33 CGKDMNGPTCC---ESGCTCKVSNQCLAPESNGKSECSKLYGCGCGKDMNGPT 89
 CC DB 168 CVGGQEDPTVYLANDGSTPSSSPATSSPPSGGGQOT-----LYGCGCGAGWTPT 222
 CC QY 90 CCGSGSTCKVSNQCL 108
 CC DB 223 TCGAPGTCVQNMVYSQCL 241
 CC
 CC RESULT 11
 CC GUNB_FUSOX STANDARD; PRT; 462 AA.
 CC AC P46236;

DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE Putative endoglucanase type B precursor (EC 3.2.1.4) (Endo-1,4-beta-glucanase) (Cellulase).
 OS Fusarium oxysporum.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Hypocreales; Mitosporic Hypocreales; Fusarium.
 OX NCBI_TaxID=5507;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95047531; PubMed=7959045;
 RA Shepherd P.O., Grant F.J., Oort P.J., Sprecher C.A., Foster D.C.,
 RA Hagen F.S., Uphall A., McKnight G.L., O'Hara P.J.;
 RT "The use of conserved cellulase family-specific sequences to clone
 RT cellulase homologue cDNAs from *Fusarium oxysporum*.";
 RL Gene 150:163-167(1994).
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-glucosidic
 CC linkages in cellulose.
 CC -1- SIMILARITY: CONTAINS 1 FUNGAL-TYPE CELLULOSE-BINDING DOMAIN (CBD).
 CC -1- SIMILARITY: BELONGS TO CELLULOSE FAMILY B (FAMILY 6 OF GLYCOSYL
 CC HYDROLASES).
 CC -----
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 CC -----
 DR EMBL: I29377; AAA6585.1; -
 DR HSSP: P07987; 1CB2.
 DR InterPro: IPR000254; CBD_fungal.
 DR InterPro: IPR001524; GH_6.
 DR Pfam: PF00734; CBM_1; 1.
 DR Pfam: PF01341; Glyco_hydro_6; 1.
 DR PRINTS: PR00733; GHYDRASE6.
 DR ProDom: PD001821; CBD_fungal; 1.
 DR ProDom: PD003733; GH_6; 1.
 DR SMART: SM00236; ECBD; 1.
 DR PROSITE: PS00562; CBD_FUNGAL; 1.
 DR PROSITE: PS00655; GLYCOSYL_HYDROL_F6_1; 1.
 DR PROSITE: PS00656; GLYCOSYL_HYDROL_F6_2; 1.
 DR Cellulose degradation; Hydrolyase; Glycosidase; Glycoprotein; Signal.
 FT SIGNAL 1 16
 FT CHAIN 17 462
 FT DOMAIN 17 65
 FT DOMAIN 66 99
 FT DOMAIN 100 462
 FT ACT_SITE 190 190
 FT ACT_SITE 236 236
 FT ACT_SITE 416 416
 FT DISULFID 33 50
 FT DISULFID 44 60
 FT DISULFID 191 250
 FT DISULFID 383 430
 FT CARBOHYD 37 37
 FT CARBOHYD 223 223
 FT CARBOHYD 272 272
 FT CARBOHYD 317 317
 FT CARBOHYD 462 AA; 49207 MW; E25B258628B637F CRC64;
 SO SEQUENCE
 Query Match 7.5%; Score 152; DB 1; Length 462;
 Best Local Similarity 34.8%; Pred. No. 0.0022;
 Matches 31; Conservative 14; Mismatches 36; Indels 8; Gaps 2;
 QY 73 CSK-LYGGCGGKDWNGPTCCSGSTCKVSNDRYQCLAPENGNKTKSAAKTTTTPA 131
 DB 25 CSNGVACCGGQNWGTPCCTSGNKCVKLNDFYSOCGSAEPSTAGPSSTAT---- 80
 QY 132 KEITTAASNSNSGKXIVSGASGN 160

Db 81 ---KTATGSSSTTAGSVTSAPPASDN 106
 RESULT 12
 ID JAG1_HUMAN STANDARD; PRT; 1218 AA.
 AC P78504; O15122; O14902; O15816;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Jagged 1 precursor (Jagged1) (Jhl).
 GN JAG1.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97422615; PubMed=9268641;
 RA Oda T., Elkanloun A.G., Meltzer P.S., Chandrasekharappa S.C.;
 RT "Identification and cloning of the human homolog (JAG1) of the rat
 RT Jagged1 gene from the Alagille syndrome critical region at 20p12.";
 RL Genomics 43:376-379(1997).
 RN [2]
 RP SEQUENCE FROM N.A., AND VARIANT AGS CVS-184.
 RC TISSUE=Bone marrow;
 RX MEDLINE=97351506; PubMed=9207788;
 RA Li L., Krantz I.D., Deng Y., Genin A., Banta A.B., Collins C.C.,
 RA Qi M., Trask B.J., Kuo W.L., Cochran J., Costa T., Pierpont M.E.M.,
 RA Rand E.B., Piccoli D.A., Hood L., Spinner N.B.;
 RT "Alagille syndrome is caused by mutations in human Jagged1, which
 RT encodes a ligand for Notch1.";
 RL Nat. Genet. 16:243-251(1997).
 RN [3]
 RP SEQUENCE FROM N.A., AND FUNCTION.
 RX MEDLINE=98122342; PubMed=9462510;
 RA Li L., Milner L.A., Deng Y., Iwata M., Banta A.B., Graf L.,
 RA Marcovina S., Friedman C., Trask B.J., Hood L., Torok-Storb B.;
 RT "The human homolog of rat Jagged1 expressed by marrow stroma inhibits
 RT differentiation of 32D cells through interaction with Notch1.";
 RL Immunity 8:43-55(1998).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Cervical carcinoma;
 RX MEDLINE=99262417; PubMed=10329625;
 RA Bash J., Zong W.-X., Banga S., Rivera A., Ballard D.W., Ron Y.,
 RA Gelinas C.;
 RT "Rel/NF-kappaB can trigger the Notch signaling pathway by inducing the
 RT expression of Jagged1, a ligand for Notch receptors.";
 RL EMBO J. 18:2803-2811(1999).
 RN [5]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99180765; PubMed=10079256;
 RA Gray G.E., Mann R.J., Mitsiadis E., Henrique D., Carcangiu M.-L.,
 RA Banks A., Leiman J., Ward D., Ish-Horowitz D., Artavanis-Tsakonas S.;
 RT "Human ligands of the Notch receptor.";
 RL Am. J. Pathol. 154:785-794(1999).
 RN [6]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21638749; PubMed=11780052;
 RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
 RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,
 RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
 RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
 RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
 RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
 RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Cotby N.R.,
 RA Coulson A.G., Coville G.J., Deadman R., Dhami P.D., Dunn M.,
 RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
 RA Gatliff D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
 RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
 RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
 RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,

RA Lehevalatlo M.H., Leverisha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
RA Marsh V.L., Martin S.L., McComachie L.J., Mclay K., McMurray A.A.,
RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
RA Oliver G., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkeen R., Sims S.,
RA Skuce C.D., Smith M.L., Sodelund C., Steward C.A., Stilson J.E.,
RA Swann R.M., Symcote N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
RA Tracey A., Tromans A.C., Vaudin M., Wali M., Wallis J.M., Williams S.A.,
RA Whitehead S.L., Whitelaker P., Willey D.L., Williams L., Williams S.A.,
RA Wilmshurst L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
RA Rogers J.;
RT "The DNA sequence and comparative analysis of human chromosome 20.";
RL Nature 414:865-871(2001).
[7]
RA SEQUENCE OF 14-1227 FROM N.A.
RC TISSUE=Umbilical vein endothelial cells;
RX MEDLINE=97115768; PubMed=9955070;
RA Zimin A.B., Pepper M.S., McMahon G.A., Nguyen F., Montesano R.,
RA Maciag T.;
RT "An antisense oligonucleotide to the notch ligand jagged enhances
RT fibroblast growth factor-induced angiogenesis in vitro.";
RL J. Biol. Chem. 271:32499-32502(1996).
[8]
RA DISEASE.
RX MEDLINE=97351505; PubMed=9207787;
RA Oda T., Elkhallouf A.G., Pike B.L., Okajima K., Krantz I.D., Genin A.,
RA Piccoli D.A., Melzer P.S., Spinner N.B., Collins F.S.,
RA Chandrasekharappa S.C.;
RT "Mutations in the human jagged1 gene are responsible for Alagille
RT syndrome.";
RL Nat. Genet. 16:235-242(1997).
[9]
RA DEVELOPMENTAL STAGE.
RX MEDLINE=20436345; PubMed=10978356;
RA Jones E.A., Clement-Jones M., Wilson D.I.;
RT "JAGGED1 expression in human embryos: correlation with the Alagille
RT syndrome phenotype.";
RL J. Med. Genet. 37:663-668(2000).
[10]
RA VARIANTS AGS CYS-184 AND HIS-184.
RX MEDLINE=98254456; PubMed=9585603;
RA Krantz I.D., Colliton R.P., Genin A., Rand E.B., Li L., Piccoli D.A.,
RA Spinner N.B.;
RT "Spectrum and frequency of jagged1 (JAG1) mutations in Alagille
RT syndrome patients and their families.";
RL Am. J. Hum. Genet. 62:1361-1369(1998).
[11]
RA VARIANTS AGS HIS-79, THR-127, ARG-129, LEU-163, GLY-184, SER-187,
RP GLY-229; PHE-284; CYS-288; PHE-338; SER-731 AND ARG-740.
RX MEDLINE=99238888; PubMed=10220506;
RA Crosnier C., Driancourt C., Raynaud-N., Dhome-Pollet S., Pollet N.,
RA Bernard O., Hadchouel M., Meunier-Rotival M.;
RT "Mutations in JAGGED1 gene are predominantly sporadic in Alagille
RT syndrome.";
RL Gastroenterology 116:1141-1148(1999).
[12]
RA VARIANTS AGS THR-152 AND LEU-184.
RX MEDLINE=20004539; PubMed=10533055;
RA Pilla G., Uda M., Macis D., Frau F., Cisponti L., Balli F.,
RA Barbera C., Colombo C., Frediani T., Gatti R., Iorle R., Marazzi M.G.,
RA Maccellini M., Musumeci S., Nebbia G., Vajro P., Ruffa G., Zancan L.,
CAO A., Devigili S.;
RT "Jagged-1 mutation analysis in Italian Alagille syndrome patients.";
RL Hum. Mutat. 14:394-400(1999).
[13]
RA VARIANTS AGS TYR-229 AND ARG-386.
RX MEDLINE=20514559; PubMed=11058898;
RA Heritege M.L., MacMillan J.C., Colliton R.P., Genin A., Spinner N.B.,
RA Anderson G.J.;
RT "Jagged1 (JAG1) mutation detection in an Australian Alagille syndrome
RT population.";
RL Hum. Mutat. 16:408-416(2000).

```

RN [14] VARIANT TOP ASP-274.
RX MEDLINE=21067871; PubMed=11152664;
RA Eladsh Z.A., Hemosh A., Bieri N.J., Montgomery R.A., Duke M.,
RA Elkins R., Dietz H.C.;
RT "Familial Tetralogy of Fallot caused by mutation in the jagged1
RT gene".
RL Hum. Mol. Genet. 10:163-169(2001).
RN [15]
RN VARIANT AGS SER-37.
RX MEDLINE=21096916; PubMed=11157803;
RA Morrisette J.D., Colliton R.P., Spilner N.B.;
RT "Defective intracellular transport and processing of JAG1 missense
RT mutations in Alagille syndrome."
RL Hum. Mol. Genet. 10:405-413(2001).
RN [16]
RN VARIANTS AGS PHE-220 AND ARG-753.
RX MEDLINE=20579880; PubMed=11139247;
RA Cromier C., Driancourt C., Raynaud N., Hachouel M.,
RA Meunier-Rotival M.;
RT "Fifteen novel mutations in the JAGGED1 gene of patients with Alagille
RT syndrome."
RL Hum. Mutat. 17:72-73(2001).
CC -1- FUNCTION: Ligand for multiple Notch receptors and involved in the
CC mediation of Notch signaling. May be involved in cell-fate
CC decisions during hematopoiesis. Seems to be involved in early
CC and late stages of mammalian cardiovascular development. Inhibits
CC myoblast differentiation (By similarity). Enhances fibroblast
CC growth factor-induced angiogenesis (in vitro).
CC -1- SUBUNIT: Interacts with NOTCH1, NOTCH2 AND NOTCH3 (By similarity).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- TISSUE SPECIFICITY: Widely expressed in adult and fetal tissues.
CC in cervix epithelium expressed in undifferentiated subcolumnar
CC reserve cells and squamous metaplasia. Expression is up-regulated
CC in cervical squamous cell carcinoma. Expressed in bone marrow cell
CC line HS-27a which supports the long-term maintenance of immature
CC progenitor cells.
CC -1- DEVELOPMENTAL STAGE: Expressed in 32-52 days embryos in the distal
CC cardiac outflow tract and pulmonary artery, major arteries, portal
CC vein, optic vesicle, otocyst, branchial arches, metanephros,
CC pancreas, mesocardium, around the major bronchial branches, and in
CC the neural tube.
CC -1- DISEASE: Defects in JAG1 are the cause of Alagille syndrome (AGS),
CC an autosomal dominant development disorder that affects structures
CC in the liver, heart, skeleton, eye, kidney, and other organs.
CC -1- DISEASE: Defects in JAG1 are associated with right heart
CC obstructive disease variants of Tetralogy of Fallot (TOF), the
CC most common form of complex congenital heart disease.
CC -1- SIMILARITY: CONTAINS 15 EGF-LIKE DOMAINS.
CC -1- SIMILARITY: CONTAINS 1 DSL DOMAIN.
CC -1- CAUTION: Ref.7 sequence differs from that shown due to a
CC framehift in position 1187.
CC CC
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CC CC
CC
CC Query Match 7.3%; Score 147.5; DB 1; Length 1218;
CC Best Local Similarity 20.9%; Pred. No. 0.011;
CC Matches 89; Conservative 36; Mismatches 159; Indels 143; Gaps 23;
CC
CC 22 SAACSKLU-----YQCGGKDKNGPTC-----GSSGTRK-VSNDDYSQCLAPSPN 66
CC Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
CC 423 NAKSKCKULIASYDCD-LPGMMGNCNDININDCLGQCNQDASCRDLVNGY--RCLCP- 477
CC
CC 67 GNKSSECSKLYGQC-----GGR-----DNMGPTCESG 94
CC Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
CC 478 GYAGDHCEKRDIDECASNPCLNGHGHCQNEIRFOCLCPGFSGNLCQLDIDVCEPFCONG 537
CC
CC 95 STC-KVSNDDYSQCLAPES-NGNNTSSBAHKTTTTPAKETTTTAKASNSNSGKYSI 152

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Db 538 AQCYNRADYFCKC--PEDYEGKNSHLKDHCRTPCEVIVISCTVAMASNDTPCEVRY-- 593
OY 153 VSGASGNGVTRRYWDCCASCSMPGKANVSPV---SCKNDGYTA-----LSDSNVQ 203
Db 594 ----ISSN-----VCGPHGCKKSOGSKFTCDCKN-GPTGYCHENINDCSN 636
OY 204 SGCNGG-----NSYMCNDNCPWA-----VNDLAVGFAAALISGGESR-----WCC 245
Db 637 PCRNNGTCTIDGVNSYKICISDMEGAYCETINND-----CSQNPCHNGTCTRDVNDPYC 691
OY 246 SCFEITFTSTVAKKMTVQVNTNGDGLSSSTGAHFDLQMPG----- 287
Db 692 DCKNMGKGTCHSRSDQDEATCNNGGTCYDGDAFKCMCPGMEGTTCNIAFNSSCLPN 751
OY 288 ----GGVGIFNG-----CSKMGAPNDMGSRYGGISASDSSLPALQAGCKRRNV 337
Db 752 PCHNGGTCVNGESFTVCCKEGMEGPICA-----QNTNDCSPHPCYNSGTCVADGNW 803
OY 338 FK 339
Db 804 YR 805

RESULT 13
JAG1 MOUSE STANDARD: PRT; 1218 AA.
ID JAG1 MOUSE
AC 090XK0;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DE 15-JUN-2002 (Rel. 41, Last annotation update)
DE Jagged 1 precursor (Jagged1).
GN JAG1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RX [1]
RP SEQUENCE FROM N.A., AND RECEPTOR INTERACTION.
RX MEDLINE=20020271; PubMed=10551863;
RA Shimizu K., Chiba S., Kumano K., Hosoya N., Takahashi T., Kanda Y.,
RA Hamada Y., Yazaki Y., Hirai H.;
RT "Mouse Jagged1 physically interacts with Notch2 and other Notch
RT receptors: assessment by quantitative methods.";
RL J. Biol. Chem. 274:32961-32969(1999).
RN [2]
RP TISSUE SPECIFICITY.
RX MEDLINE=20025753; PubMed=10556292;
RA Loomes K.M., Underkofler L.A., Morabito J., Gottlieb S.,
RA Piccoli D.A., Spinner N.B., Baldwin H.S., Oakey R.J.;
RT "The expression of Jagged1 in the developing mammalian heart
RT correlates with cardiovascular disease in Alagille syndrome.";
RL Hum. Mol. Genet. 8:2443-2449(1999).
CC -1- FUNCTION: Ligand for multiple Notch receptors and involved in the
CC mediation of Notch signaling. May be involved in cell-fate
CC decisions during hematopoiesis. Seems to be involved in early
CC and late stages of mammalian cardiovascular development. Inhibits
CC myoblast differentiation (By similarity). May regulate fibroblast
CC growth factor-induced angiogenesis.
CC -1- SUBUNIT: Interacts with NOTCH1, NOTCH2 AND NOTCH3.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- TISSUE SPECIFICITY: Widely expressed in many tissues, with highest
CC expression in brain, heart, muscle and thymus.
CC -1- DEVELOPMENTAL STAGE: At 8.75-9.75 d.p.c. expression was detected
CC in structures that include those destined to contribute to the
CC cardiovascular system of the adult heart. Expression was also
CC detected in the mesencephalon and rhombencephalon.
CC -1- DOMAIN: The DSL domain is indispensable and sufficient for binding
CC to NOTCH2.
CC -1- SIMILARITY: CONTAINS 15 EGF-LIKE DOMAINS.
CC -1- SIMILARITY: CONTAINS 1 DSL DOMAIN.

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CC -----
CC EMBL; AF11092; AAF15505.1; -.
CC HSSP; P00740; 1EDM.
CC MED; MGI:1095416; Jag1.
CC InterPro; IPR000152; Asx_hydroxyl.
CC InterPro; IPR001774; DSL.
CC InterPro; IPR000561; EGF-like.
CC InterPro; IPR000742; EGF 2.
CC InterPro; IPR001881; EGF Ca.
CC InterPro; IPR001438; EGF-11.
CC InterPro; IPR002049; laminin_EGF.
CC InterPro; IPR010071; WVF_C.
CC Pfam; PF01414; DSL; 1.
CC Pfam; PF00008; EGF; 14.
CC PRINTS; PR00010; EGFBL00D.
CC PRINTS; PR00011; EGFAMININ.
CC SMART; SM00051; DSL; 1.
CC SMART; SM00179; EGF_CA; 10.
CC SMART; SM00001; EGF_Like; 6.
CC SMART; SM00214; VWC; 1.
CC PROSITE; PS00010; ASX_HYDROXYL; 10.
CC PROSITE; PS00022; EGF_1; 16.
CC PROSITE; PS01186; EGF_2; 12.
CC PROSITE; PS01187; EGF_CA; 8.
CC KMW Calcium-binding; EGF-like domain; Glycoprotein; Developmental protein;
CC Repeat; Transmembrane; Signal.
CC FT SIGNAL 1 33
CC FT CHAIN 34 1218
CC FT DOMAIN 34 1067
CC FT TRANSMEM 1068 1093
CC FT 1094 1218
CC FT DOMAIN 167 229
CC FT DOMAIN 230 266
CC FT DOMAIN 296 334
CC FT DOMAIN 336 372
CC FT DOMAIN 374 410
CC FT DOMAIN 412 448
CC FT DOMAIN 450 485
CC FT DOMAIN 487 523
CC FT DOMAIN 525 561
CC FT DOMAIN 574 627
CC FT DOMAIN 629 665
CC FT DOMAIN 667 703
CC FT DOMAIN 705 741
CC FT DOMAIN 744 780
CC FT DOMAIN 782 818
CC FT DOMAIN 820 856
CC FT DISULFID 300 312
CC FT DISULFID 306 322
CC FT DISULFID 324 333
CC FT DISULFID 340 351
CC FT DISULFID 345 360
CC FT DISULFID 362 371
CC FT DISULFID 378 389
CC FT DISULFID 383 398
CC FT DISULFID 400 409
CC FT DISULFID 416 427
CC FT DISULFID 421 436
CC FT DISULFID 438 447
CC FT DISULFID 454 464
CC FT DISULFID 458 473
CC FT DISULFID 475 484
CC FT DISULFID 491 502
CC FT DISULFID 496 511
CC FT DISULFID 513 522
CC FT DISULFID 529 540

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FT DISULFID 534 549 BY SIMILARITY.
 FT DISULFID 551 560 BY SIMILARITY.
 FT DISULFID 578 605 BY SIMILARITY.
 FT DISULFID 599 615 BY SIMILARITY.
 FT DISULFID 617 626 BY SIMILARITY.
 FT DISULFID 633 644 BY SIMILARITY.
 FT DISULFID 638 653 BY SIMILARITY.
 FT DISULFID 655 664 BY SIMILARITY.
 FT DISULFID 671 682 BY SIMILARITY.
 FT DISULFID 676 691 BY SIMILARITY.
 FT DISULFID 693 702 BY SIMILARITY.
 FT DISULFID 709 720 BY SIMILARITY.
 FT DISULFID 714 729 BY SIMILARITY.
 FT DISULFID 731 740 BY SIMILARITY.
 FT DISULFID 748 759 BY SIMILARITY.
 FT DISULFID 753 768 BY SIMILARITY.
 FT DISULFID 770 779 BY SIMILARITY.
 FT DISULFID 786 797 BY SIMILARITY.
 FT DISULFID 791 806 BY SIMILARITY.
 FT DISULFID 808 817 BY SIMILARITY.
 FT DISULFID 824 835 BY SIMILARITY.
 FT DISULFID 829 844 BY SIMILARITY.
 FT DISULFID 846 855 BY SIMILARITY.
 FT CARBOHYD 143 143 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 217 217 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 382 382 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 559 559 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 745 745 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 960 960 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 991 991 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1045 1045 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1064 1064 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 1218 AA; 134163 MW; 77739F89288B793C C3C64;

Query Match 7.3%; Score 147.5; DB 1; Length 1218;
 Best Local Similarity 20.9%; Pred. No. 0.011;
 Matches 89; Conservative 39; Mismatches 147; Indels 151; Gaps 24;

QY 22 SAACSKL-----YQCGGKDMNGPTC-----CESSGTRK-VSNDVYSQCLAPESN 66
 DB 423 NARSKKNLIASYYCDC-LPGWMGQNCNDINDCIQCONDASCRLVNGY--RCLCP-- 477
 QY 67 GNKSESEKLYGQC-----CGK-----DMNGPTCESSG 94
 DB 478 GYAGDHCRDRIDECAINPCLANGHCONEINRQCLCPGFSNLCOLDIDICEPPCQNG 537
 QY 95 STC-KVSNDDVYSQCLAPES-NGNKTSESAHKTITTTAPAKEITTTAKASNSNSGKY-- 150
 DB 538 AQCVRASADYFCCK--PEDYEGKNSHLKDHCRITTCETVIDSCIVAMASNDTPBEGVRIYS 595
 QY 151 SIYSG-----GASGNVYTRVYDCCCKASCSWPKAANVSPVKSCKNGVTAALSDSNVOS 204
 DB 596 SNVCGPHGKCKSOSGKFTC--DCKNKPRTGYCHEINDESNCKNGGTCI----- 645
 QY 205 GCGNGSNYMCNDNQFMA-----VND--NLAYGPAALAI-----SGGSESRWCC 245
 DB 646 --DGNVSTKICICSDMEGAHCENNNINDCSQNPCHYGTCRDUVNDPYCDCKRGMKGKTC 703
 QY 246 S-----CFELTFTSTSVAKKXWVIQVNTNGDLSSTGAHFDLQMBG----- 287
 DB 704 SRDSCDEAT-----CNGGTCYDEVDT-FKCMCGGMEGTTCNTIARRSS 747
 QY 288 -----GGVGIENG-----CSKQWGAIPNDGMSRIGGIS3ASDCSLPALQAGCKW 333
 DB 748 CLPNCHNGGTCIVVNGDSFTVCYCKEGBWGPFI-----CTQYNTDCSPHPCYNSTGTCVD 799
 QY 334 RPNWFK 339
 DB 800 GDNWTR 805

RESULT 14
 Y136_TREPA

ID Y136 TREPA STANDARD; PRT; 485 AA.
 AC 083172;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hypothetical Lipoprotein TP0136 precursor.
 GN TP0136.
 OS Treponema pallidum.
 OC Bacteria; Spirochaetales; Spirochaetaceae; Treponema.
 OX NCBI_TaxID:160;
 RN [1]
 RP SEQUENCE FROM N. A.
 RC STRAIN=Nichols;
 RX MEDLINE=98332770; PubMed=965876;
 RA Fraser C.M., Norris S.J., Weinstock G.M., White O., Sutton G.G.,
 RA Dodson R., Gwin M., Hickey E.K., Clayton R., Kechum K.A.,
 RA Sodergren E., Hardham J.M., McLeod M.P., Salzberg S., Peterson J.,
 RA Khailak H., Richardson D., Howell J.K., Chidambaram M., Utterback T.,
 RA McDonald L., Artlach P., Bowman C., Cotton M.D., Fujii C., Garland S.,
 RA Hatch B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.O.,
 RA Venter J.C.;
 RA "Complete genome sequence of Treponema pallidum, the syphilis
 agent."
 RT Spirochete.
 RL Science 281:375-388(1998).
 CC -1- SUBCELLULAR LOCATION: Attached to the membrane by a lipid anchor
 (Potential).
 CC -1- SIMILARITY: BELONGS TO THE TP013X FAMILY OF LIPOPROTEINS.
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 CC -----
 DR EMBL; AE001199; AAC65137.1; ALT_INIT.
 DR TIGR; TP0136; .
 KW Hypothetical protein; Lipoprotein; Membrane; Signal;
 KW Complete proteome.
 FT SIGNAL 1 23
 FT CHAIN 24 485
 FT LIPID 24 24 N-ACYL DIGLYCERIDE (POTENTIAL).
 FT DOMAIN 164 178 GLY/SER-RICH.
 FT DOMAIN 196 210 GLY/SER-RICH.
 FT DOMAIN 253 267 GLY/SER-RICH.
 FT DOMAIN 318 327 POLY-SER.
 FT DOMAIN 444 447 POLY-SER.
 SQ SEQUENCE 485 AA; 48984 MW; C7A4CEDEC7DC5CED CRC64;

Query Match 7.2%; Score 145; DB 1; Length 485;
 Best Local Similarity 21.7%; Pred. No. 0.0068;
 Matches 75; Conservative 43; Mismatches 131; Indels 96; Gaps 12;

QY 27 SKLY-----GQCGGKDMNGPTCESSGTCVSNDDVYSQCLAPESNGKSESEKLYGQCGGK 83
 DB 56 SKLYATNRRLMEKELNGSQWQYSSSVPPDSDKWMSINTDGTFF----- 103
 QY 84 DMNGPTCESSGTCVSNDDVYSQCLAPESNGKTSSEAHKTITTTAPAKEITTTAKASNS 143
 DB 104 -----LACVPTGTVYKHCY-----NGAGSS-----STGTTASPESTE-TCSGHATLV 143
 QY 144 SNSSGKTVISVGASGNGVTRVYDCCCKASCSWPKAANVSPVKSCKNGVTAALSDSNVQ 203
 DB 144 GGTSPFALVPGGTGNNG-----NCGCGGGGSSSSSSSCTIHWLVPGGTGNNGN 194
 QY 204 GCGNGSNYMCNDNQFMAVNDNLAYGFAAAAISGGSESRWCCCFELTFTSTV-----AG 259
 DB 195 GCGGG-----GGSSSSSSSCTIHWLVNTDEQFLMG 227
 QY 260 KRWVIQVNTNGDLSSTGAHFDLQMBGSGVIFNGCSKQWGAIPNDGMSRIGGISASD 319
 DB 228 EGYVVTTHGLVTKNGSSSAG--PAQCPGGGG-----GSSGCGGSSSEYTVASCSF 276

QY 320 CSSLSALQAGCKMFPNMFKNADNSMTYKVTCPKEITAKTCCS 364
 Db 277 STPIIASVSDGC---YHYI-----LTREKVCYCRKODTASSAAS 311

RESULT 15
 JAG1_BRARE STANDARD, PRT, 1242 AA.
 AC 090Y57;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DE Jagged 1 precursor (Jagged1).
 GN JAG1.
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OX NCBI_Taxid=7955;
 RN (1)
 RP SEQUENCE FROM N.A.
 RA Oda T., Chandrasekharappa S.C.;
 RT "Isolation, characterization and expression analysis of Zebrafish
 RT Jagged genes";
 RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Ligand for multiple Notch receptors and involved in the
 CC mediation of Notch signaling (By similarity). Seems to be involved
 CC in cell-fate decisions.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
 CC -1- SIMILARITY: CONTAINS 17 EGF-LIKE DOMAINS.
 CC -1- SIMILARITY: CONTAINS 1 DSL DOMAIN.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
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 CC -----
 CC DR EMBL; AF229448; AL08213.1; -
 CC DR ZFIN; ZDB-GENE-011128-2; JAG1.
 CC DR InterPro; IPR000152; Asx_hydroxyl.
 CC DR InterPro; IPR001774; DSL.
 CC DR InterPro; IPR000561; EGF-like.
 CC DR InterPro; IPR000742; EGF 2.
 CC DR InterPro; IPR001881; EGF_Ca.
 CC DR Pfam; PF01414; DSL; 1.
 CC DR Pfam; PF00008; EGF; 18.
 CC DR PROSITE; PS00010; ASX_HYDROXYL; 9.
 CC DR PROSITE; PS00022; EGF 1; 16.
 CC DR PROSITE; PS01186; EGF 2; 12.
 CC DR PROSITE; PS01187; EGF_Ca; 8.
 CC DR PROSITE; PS01187; EGF_Ca; 8.
 CC KW Calcium-binding; EGF-like domain; Glycoprotein; Developmental protein;
 CC Repeat; Transmembrane; Signal.
 CC FT SIGNAL 1 28
 CC FT CHAIN 29 1242
 CC FT DOMAIN 29 1070
 CC FT TRANSMEM 1071 1095
 CC FT DOMAIN 1096 1242
 CC FT DOMAIN 168 220
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 CC FT DOMAIN 265 295
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 CC FT DOMAIN 488 524
 CC FT DOMAIN 526 562
 CC FT DOMAIN 565 630
 CC FT DOMAIN 632 666
 CC EGF-LIKE 1.
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 CC EGF-LIKE 4.
 CC EGF-LIKE 5.
 CC EGF-LIKE 6.
 CC EGF-LIKE 7.
 CC EGF-LIKE 8.
 CC EGF-LIKE 9.
 CC EGF-LIKE 10.
 CC EGF-LIKE 11, CALCIUM-BINDING (POTENTIAL).

FT DOMAIN 670 706 EGF-LIKE 12, CALCIUM-BINDING (POTENTIAL).
 FT DOMAIN 708 744 EGF-LIKE 13.
 FT DOMAIN 747 783 EGF-LIKE 14.
 FT DOMAIN 785 821 EGF-LIKE 15, CALCIUM-BINDING (POTENTIAL).
 FT DOMAIN 823 859 EGF-LIKE 16, CALCIUM-BINDING (POTENTIAL).
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Query Match 7.2%; Score 145; DB 1; Length 1242;
 Best Local Similarity 21.1%; Pred. No. 0.017;
 Matches 82; Conservative 45; Mismatches 142; Indels 120; Gaps 22;

QY 32 OCGGND-WNGPTC-----CEGSGTCK-VSNPYSGCLAPESNGNSSECSKLYG 78
 Db 655 QCICADGMEGPNVCEETNIDDCRTNPRDRGVCRDLVNDYCEC-----EWGKGTCHSRES 710
 QY 79 QC-----GG-----KDWNGPTC-----CEGSGTCKVSNPYYS 105
 Db 711 QCDEDTGNNGTGCSDEBGDSFCKLCSFGMEGATCNIAKNSCLPPECNGATCVTGDGFT 770

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